

Dsg3 Cas9-KO Strategy

Designer:Xueting Zhang

Project Overview



Project Name

Dsg3

Project type

Cas9-KO

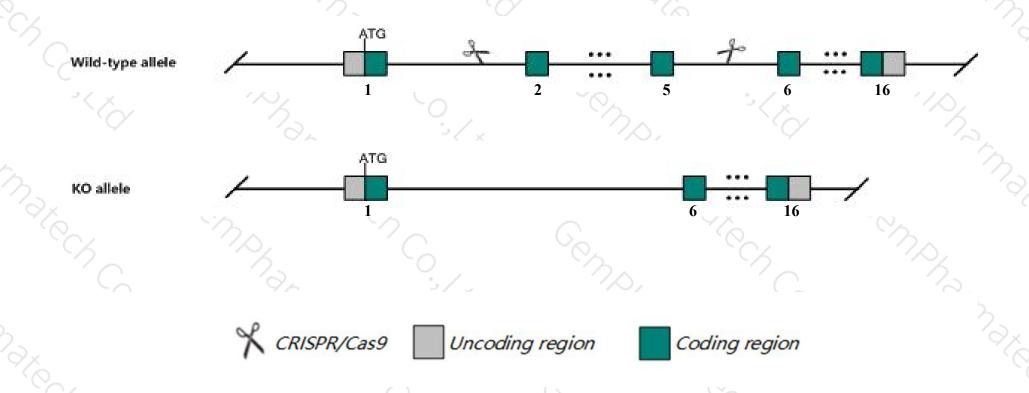
Strain background

C57BL/6JGpt

Knockout strategy



This model will use CRISPR/Cas9 technology to edit the *Dsg3* gene. The schematic diagram is as follows:



Technical routes



- ➤ The *Dsg3* gene has 2 transcripts. According to the structure of *Dsg3* gene, exon2-exon5 of *Dsg3-201*(ENSMUST00000070892.7) transcript is recommended as the knockout region. The region contains 469bp coding sequence.

 Knock out the region will result in disruption of protein function.
- ➤ In this project we use CRISPR/Cas9 technology to modify *Dsg3* gene. The brief process is as follows: CRISPR/Cas9 system

Notice



- ➤ According to the existing MGI data, Homozygous mutants display runting from decreased food intake due to oropharyngeal epithelial lesions, blisters around snout and eyes, hair loss by weaning, and hair regrowth with bald patches throughout life.
- > The *Dsg3* gene is located on the Chr18. If the knockout mice are crossed with other mice strains to obtain double gene positive homozygous mouse offspring, please avoid the two genes on the same chromosome.
- This Strategy is designed based on genetic information in existing databases. Due to the complexity of biological processes, all risk of the gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

Gene information (NCBI)



Dsg3 desmoglein 3 [Mus musculus (house mouse)]

Gene ID: 13512, updated on 31-Jan-2019

Summary

Official Symbol Dsg3 provided by MGI

Official Full Name desmoglein 3 provided by MGI

Primary source MGI:MGI:99499

See related Ensembl:ENSMUSG00000056632

Gene type protein coding RefSeq status REVIEWED Organism

Mus musculus

Lineage Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha;

Muroidea; Muridae; Murinae; Mus; Mus

Also known as

This gene encodes a member of the cadherin family of proteins that forms an integral transmembrane component of desmosomes, the

multiprotein complexes involved in cell adhesion, organization of the cytoskeleton, cell sorting and cell signaling. The encoded preproprotein undergoes proteolytic processing to generate a mature, functional protein. Mice lacking the encoded protein exhibit loss of keratinocyte cell adhesion resulting in a phenotype that resembles that of patients with pemphigus vulgaris. This gene is located in a cluster of desmosomal

cadherin genes on chromosome 18. [provided by RefSeq, Feb 2016]

Expression Biased expression in stomach adult (RPKM 2.1), lung adult (RPKM 1.0) and 4 other tissuesSee more

Orthologs <u>human all</u>

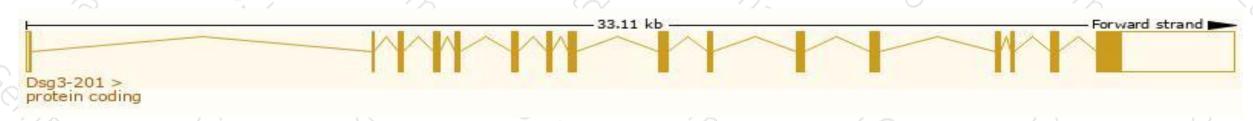
Transcript information (Ensembl)



The gene has 2 transcripts, all transcripts are shown below:

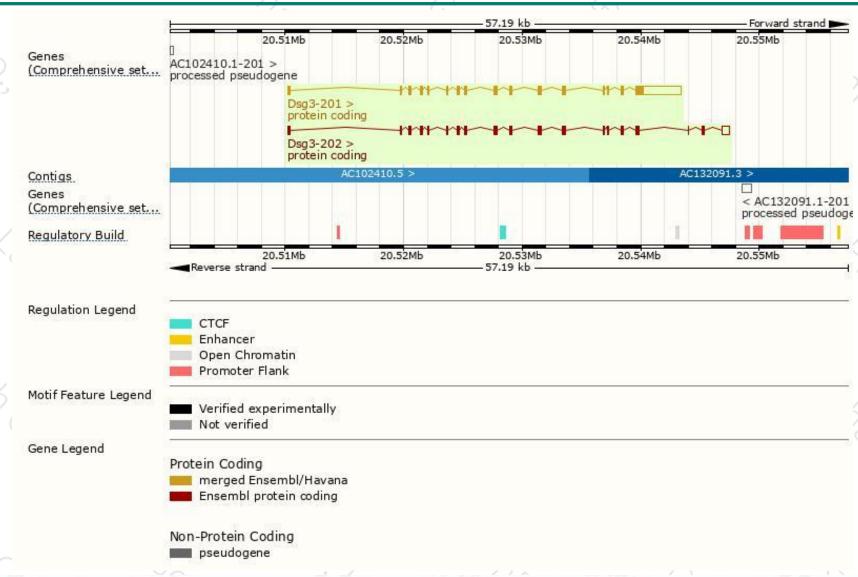
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Dsg3-201	ENSMUST00000070892.7	6212	993aa	Protein coding	CCDS29083	Q3UFC6	TSL:1 GENCODE basic APPRIS P2
Dsg3-202	ENSMUST00000234945.1	3482	929aa	Protein coding	353	350	GENCODE basic APPRIS ALT2

The strategy is based on the design of *Dsg3-201* transcript, The transcription is shown below



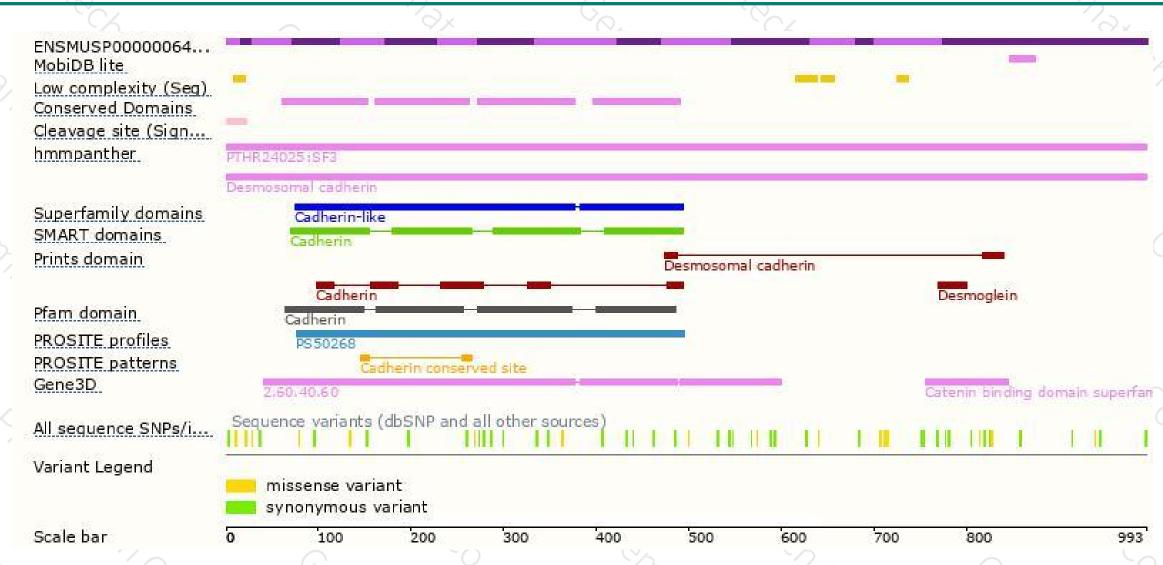
Genomic location distribution





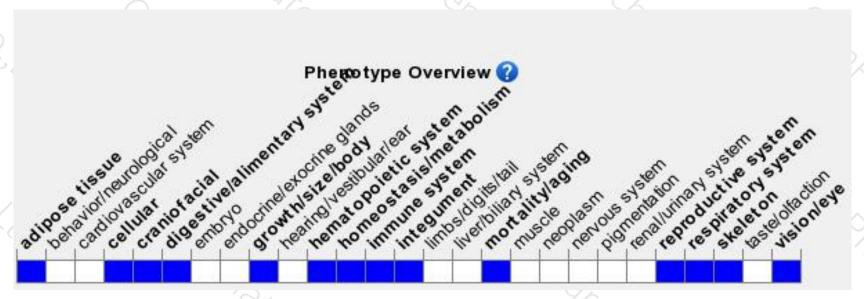
Protein domain





Mouse phenotype description(MGI)





Phenotypes affected by the gene are marked in blue.Data quoted from MGI database(http://www.informatics.jax.org/).

According to the existing MGI data, Homozygous mutants display runting from decreased food intake due to oropharyngeal epithelial lesions, blisters around snout and eyes, hair loss by weaning, and hair regrowth with bald patches throughout life.



If you have any questions, you are welcome to inquire. Tel: 400-9660890





